

Amendments to the Specification:

Please replace the first paragraph after the title (lines 3-5) with the following paragraph:

This application is the National Stage application of PCT/DK2004/000478 filed on July 2, 2004, which claims benefit to Danish Application No. PA 2003 01010 filed on July 3, 2003 and U.S. provisional Application No. 60/484,923, filed July 3, 2003 (now expired), which application(s) are incorporated herein by reference.

Please replace the third paragraph on page 17, lines 20-24, with the following paragraph:

Pfam consensus: a consensus sequence derived from a large collection of protein multiple sequence alignments and profile hidden Markov models used to identify conserved protein domains (Bateman *et al.*, 2002, Nucleic Acids Res. 30: 276-80; and searchable on <http://www.theinternetatsanger.ac.uk/Software/Pfam/> and on NCBI at <http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>.

Please replace the fourth paragraph on page 17, lines 26-30, with the following paragraph:

Protein domain prediction: sequences are analyzed by BLAST (www.ncbi.nlm.nih.gov/BLAST/) and PredictProtein (www.emblheidelberg.de/predictprotein/predictprotein). Signal peptides are predicted by SignalP v. 1.1 (www.cbs.dtu.dk/services/signalP/) and transmembrane regions are predicted by TMHMM v. 2.0 (www.cbs.dtu.dk/services/TMHMM/).

Please replace the paragraph on page 19, lines 19-31 through page 20, lines 1-4, with the following paragraph:

Substantially identical: refers to two nucleic acid or polypeptide sequences that have at least about 60%, preferably about 65%, more preferably about 70%, further more preferably about 80%, most preferably about 90 or about 95% nucleotide or amino acid residue identity when aligned for maximum correspondence over a comparison window as measured using one of the sequence comparison algorithms given herein, or by manual alignment and visual inspection. This definition also refers to the complement of the test sequence with respect to its substantial identity to a reference sequence. A comparison window refers to any one of the number of contiguous positions in a sequence (being anything from between about 20 to about 600, most commonly about 100 to about 150) which may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Optimal alignment can be achieved using computerized implementations of alignment algorithms (e.g., GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis. USA) or BLAST analyses available on the site: (www.ncbi.nlm.nih.gov/) (ncbi.nlm.nih.gov/)

Please replace the paragraph on page 53, lines 5-21, with the following:

The *NFR5* Nod-factor binding proteins encoded by the *NFR5* alleles of *Lotus japonicus* ecotype GIFU (gene sequence: SEQ ID No: 7; protein sequence: SEQ ID No: 24 & 25), and *Lotus filicaulis* (gene sequence SEQ ID No: 30; protein sequence SEQ ID No: 31) have been compared, and found to show diversity in their primary structure. Using the sequence information available for the *Lotus NFR5* gene together with the pea SYM10 gene (Table 12), the alleles from different ecotypes or varieties of *Lotus*, pea and other legumes can now be identified, and used directly in breeding programs. By further way of example, the nucleic acid sequence of the *Phaseolus vulgaris NFR5* gene (SEQ ID No: 39) has facilitated the identification of a molecular marker for two different *NFR5* alleles in the *Phaseolus vulgaris* lines Bat93 and Jalo EEP558, that is based on a single nucleotide difference creating an *ApoI* restriction site (RAATTY) in line Bat93, wherein R stands for A or G, Y for C or T. A partial sequence of the *NFR5* gene comprising the *ApoI* site molecular marker identified in line Bat93 is shown in bold type:

CACAGGACATATTGAGTGAAAACAACATGGTCAA**AATTT**CACTGCCGC
AAGCAACCTTCCAGTTT**T**GATCCCAGTTACA (SEQ ID No: 55)

Please replace the paragraph on page 53, lines 22-25, with the following:

The absence of this Apol site in the comparable *NFR5* partial sequence of line Jalo EEP558 is shown in bold type:

CACAGGACATATTGAGTGAAAACAACATGGTCAA**AATTT**CACTGCCGC
AAGCAACCTTCCAGTTT**T**GATCCCAGTTACA (SEQ ID No: 56)

Please replace Table 1 on page 55 with the following:

Table 1

Alignment of *Lotus*, *Glycine* and *Phaseolus* NFR5 protein sequences

		1	2	3	4	50	
<i>Lotus</i>		1	2	3	4	50	
<i>Glycine</i>		1	2	3	4	50	
<i>Phaseolus</i>		1	2	3	4	50	
		6	7	8	9	100	
<i>Lotus</i>		6	7	8	9	100	
<i>Glycine</i>		6	7	8	9	100	
<i>Phaseolus</i>		6	7	8	9	100	
		11	12	13	14	150	
<i>Lotus</i>		11	12	13	14	150	
<i>Glycine</i>		11	12	13	14	150	
<i>Phaseolus</i>		11	12	13	14	150	
		16	17	18	19	200	
<i>Lotus</i>		16	17	18	19	200	
<i>Glycine</i>		16	17	18	19	200	
<i>Phaseolus</i>		16	17	18	19	200	
		21	22	23	24	250	
<i>Lotus</i>		21	22	23	24	250	
<i>Glycine</i>		21	22	23	24	250	
<i>Phaseolus</i>		21	22	23	24	250	
		26	27	28	29	300	
<i>Lotus</i>		26	27	28	29	300	
<i>Glycine</i>		26	27	28	29	300	
<i>Phaseolus</i>		26	27	28	29	300	
		31	32	33	34	350	
<i>Lotus</i>		31	32	33	34	350	
<i>Glycine</i>		31	32	33	34	350	
<i>Phaseolus</i>		31	32	33	34	350	
		36	37	38	39	400	
<i>Lotus</i>		36	37	38	39	400	
<i>Glycine</i>		36	37	38	39	400	
<i>Phaseolus</i>		36	37	38	39	400	
		41	42	43	44	450	
<i>Lotus</i>		41	42	43	44	450	
<i>Glycine</i>		41	42	43	44	450	
<i>Phaseolus</i>		41	42	43	44	450	
		46	47	48	49	500	
<i>Lotus</i>		46	47	48	49	500	
<i>Glycine</i>		46	47	48	49	500	
<i>Phaseolus</i>		46	47	48	49	500	
		51	52	53	54	550	
<i>Lotus</i>		51	52	53	54	550	
<i>Glycine</i>		51	52	53	54	550	
<i>Phaseolus</i>		51	52	53	54	550	
		56	57	58	59	600	
<i>Lotus</i>		56	57	58	59	600	
<i>Glycine</i>		56	57	58	59	600	
<i>Phaseolus</i>		56	57	58	59	600	
		61	62	63	64	650	
<i>Lotus</i>		61	62	63	64	650	SEQ ID NO: 1
<i>Glycine</i>		61	62	63	64	650	SEQ ID NO: 2
<i>Phaseolus</i>		61	62	63	64	650	SEQ ID NO: 3

Please replace Table 3 on page 57 with the following:

Table 3

Alignment of *Lotus* and *Pisum* NFR1 protein sequences

	1	5	10	15	20	25	30	35	40	45	50
<i>Pisum</i>	1	MDLAKSLLAR	F
<i>Pisum</i>	1	MDLAKSLLAR	F
<i>Lotus</i>	1	MDLAKSLLAR	F
<i>Pisum</i>	5	TPMGRSLVH	SRVYVYH
<i>Pisum</i>	5	TPMGRSLVH	SRVYVYH
<i>Lotus</i>	5	TPMGRSLVH	SRVYVYH
<i>Pisum</i>	10	HYFTYTHAG	DTYTLTANG
<i>Pisum</i>	10	HYFTYTHAG	DTYTLTANG
<i>Lotus</i>	10	HYFTYTHAG	DTYTLTANG
<i>Pisum</i>	15	YVDSGMSQ	SDVGLSTYH
<i>Pisum</i>	15	YVDSGMSQ	SDVGLSTYH
<i>Lotus</i>	15	YVDSGMSQ	SDVGLSTYH
<i>Pisum</i>	20	PSKQSTVTP	YGRNNSKAY
<i>Pisum</i>	20	PSKQSTVTP	YGRNNSKAY
<i>Lotus</i>	20	PSKQSTVTP	YGRNNSKAY
<i>Pisum</i>	25	CHVYVTHQ	HSRSLTSS
<i>Pisum</i>	25	CHVYVTHQ	HSRSLTSS
<i>Lotus</i>	25	CHVYVTHQ	HSRSLTSS
<i>Pisum</i>	30	TAULNTHK	STFTSTHAG
<i>Pisum</i>	30	TAULNTHK	STFTSTHAG
<i>Lotus</i>	30	TAULNTHK	STFTSTHAG
<i>Pisum</i>	35	PALEKQVDA	STPLSTHAG
<i>Pisum</i>	35	PALEKQVDA	STPLSTHAG
<i>Lotus</i>	35	PALEKQVDA	STPLSTHAG
<i>Pisum</i>	40	SHLQSTHAG	STPLSTHAG
<i>Pisum</i>	40	SHLQSTHAG	STPLSTHAG
<i>Lotus</i>	40	SHLQSTHAG	STPLSTHAG
<i>Pisum</i>	45	SHLQSTHAG	STPLSTHAG
<i>Pisum</i>	45	SHLQSTHAG	STPLSTHAG
<i>Lotus</i>	45	SHLQSTHAG	STPLSTHAG
<i>Pisum</i>	50	SHLQSTHAG	STPLSTHAG
<i>Pisum</i>	50	SHLQSTHAG	STPLSTHAG
<i>Lotus</i>	50	SHLQSTHAG	STPLSTHAG
<i>Pisum</i>	55	SHLQSTHAG	STPLSTHAG
<i>Pisum</i>	55	SHLQSTHAG	STPLSTHAG
<i>Lotus</i>	55	SHLQSTHAG	STPLSTHAG
<i>Pisum</i>	60	SHLQSTHAG	STPLSTHAG
<i>Pisum</i>	60	SHLQSTHAG	STPLSTHAG
<i>Lotus</i>	60	SHLQSTHAG	STPLSTHAG

Please replace Table 11 on page 64 with the following:

TABLE 11				
Marker	Genetic distance from NFR5 locus	<u>Molecular markers for NFR5 allele breeding in Lotus</u>		SEQ ID NO:
		<u>Lotus</u> Ecotype	<u>Microsatellite sequence</u>	
TM0272	2.9 cM	MG-20	18xCT	
		Gifu	12xCT	
TM0257	1.0 cM	MG-20	10xAAG	
		Gifu	7xAAG	
LjT13i23Sfi		Gifu	TTTTGCTGCAGCAAGTCGACTGTTAGAGGA	57
		Fili	TTTTGCTGCAACAAGTCGGACTGTTAGAGGA	58
TM0522	0 cM	MG-20	24xAT	
		Gifu	14xAT	
NFR5				
E32M54-12F	0.5 cM	MG-20	TTGGAAGTTCCTTTTATTAGGTTAATTTTA	59
		Fili	TTGGAAGTTCCTTTTA - - - GGTTAATTTTA	60
LJt01C03 Not	0.7 cM	Fili	CATTCCAGAAGAAAATAAGATATAAATTATG	61
		MG-20	CATTCCAGAAGAAAATAAGATATAAATTATG	61
		Gifu	CATTCCAGAAG - AAATAAGATATAAATTATG	62
TM0168	2.2 cM	MG-20	19xAT	
		Gifu	15xAT	
TM0021	3.8 cM	MG-20	16xCT	
		Gifu	13xCT	

Please replace Table 12 on page 65 with the following:

Table 12

**Nucleotide sequence variation between the pea *SYM10* alleles
of pea cultivars Frisson and Finale***

Frisson	CTTGCAATTC	TTCACAATTT	CACAACAATG	GCTATCTTCT	TTCTTCCTTC
Finale	CTTGCAATTC	TTCACAATTT	CACAACAATG	GCTATCTTCT	TTCTTCCTTC
Frisson	TAGTTCTCAT	GCCTTTTTC	TTGCACATCAT	GTTTTTGTGTC	ACTAATATTT
Finale	TAGTTCTCAT	GCCTTTTTC	TTGCACATCAT	GTTTTTGTGTC	ACTAATATTT
Frisson	CAGCTCAACC	ATTACAACCT	AGTGAACAA	ACTTTTCATG	CCCGGTGGAT
Finale	CAGCTCAACC	ATTACAACCT	AGTGAACAA	ACTTTTCATG	CCCGGTGGAT
Frisson	TCACCTCCTT	CATGTGAAAC	CTATGTGACA	TACTTTGCTC	GGTCTCCAAA
Finale	TCACCTCCTT	CATGTGAAAC	CTATGTGACA	TACTTTGCTC	GGTCTCCAAA
Frisson	CTTTTGTGAGC	CTAACTAACA	TATCAGATAT	ATTGTGATG	AGTCCTTTAT
Finale	CTTTTGTGAGC	CTAACTAACA	TATCAGATAT	ATTGTGATG	AGTCCTTTAT
Frisson	CCATTGCAAA	AGCCAGTAAC	ATAGAAGATG	AGGACAAGAA	GCTGGTTGAA
Finale	CCATTGCAAA	AGCCAGTAAC	ATAGAAGATG	AGGACAAGAA	GCTGGTTGAA
Frisson	GGCCAAGTCT	TACTCATACC	TGTAACITGT	GSTTGCACTA	GAAATCGCTA
Finale	GGCCAAGTCT	TACTCATACC	TGTAACITGT	GSTTGCACTA	GAAATCGCTA
Frisson	TTTGCGAAT	TTCACTGACA	CAATCAAGCT	AGGTGACAAC	TATTTTCATAG
Finale	TTTGCGAAT	TTCACTGACA	CAATCAAGCT	AGGTGACAAC	TATTTTCATAG
Frisson	TTTCAACCAC	TTCATACCAG	AATCTTACAA	ATTATGTGGA	AATGGAAAAT
Finale	TTTCAACCAC	TTCATACCAG	AATCTTACAA	ATTATGTGGA	AATGGAAAAT
Frisson	TTCAACCCTA	ATCTAAGTCC	AAATCTATTG	CCACCAGAAA	TCAAAGTTGT
Finale	TTCAACCCTA	ATCTAAGTCC	AAATCTATTG	CCACCAGAAA	TCAAAGTTGT
Frisson	TGTCCCTTTA	TTCTGCAAAAT	GCCCCCTGAA	GAATCAGTTG	AGCAAAGGAA
Finale	TGTCCCTTTA	TTCTGCAAAAT	GCCCCCTGAA	GAATCAGTTG	AGCAAAGGAA
Frisson	TAAAGCATCT	GATTACTTAT	GTGTGGCAGG	CTAATGACAA	TGTTACCGGT
Finale	TAAAGCATCT	GATTACTTAT	GTGTGGCAGG	CTAATGACAA	TGTTACCGGT
Frisson	GTAAAGTTCCA	AGTTTGGTGC	ATCACAAGTG	GATATGTTTA	CTGAAAACAA
Finale	GTAAAGTTCCA	AGTTTGGTGC	ATCACAAGTG	GATATGTTTA	CTGAAAACAA
Frisson	TCAAAACTTC	ACTGCTTCAA	CCAAAGTTCC	GATTTTGATC	CCTGTGACAA
Finale	TCAAAACTTC	ACTGCTTCAA	CCAAAGTTCC	GATTTTGATC	CCTGTGACAA
Frisson	AGTTACCGGT	AATTGATCAA	CCATCTTCAA	ATGGAAGAAA	AAACAGCACT
Finale	AGTTACCGGT	AATTGATCAA	CCATCTTCAA	ATGGAAGAAA	AAACAGCACT

Frission	CAAAAACCTG	CTTTTATAAT	TGGTATTAGC	CTAGGATGTG	CTTTTTTCGT
Finale	CAAAAACCTG	CTTTTATAAT	TGGTATTAGC	CTAGGATGTG	CTTTTTTCGT
Frission	TGTAGTTTTA	ACACTATCAC	TTGTTTATGT	ATATTGTCTG	AAAATGAAGA
Finale	TGTAGTTTTA	ACACTATCAC	TTGTTTATGT	ATATTGTCTG	AAAATGAAGA
Frission	GATTGAATAG	GAGTACTTCA	TTGGCGGAGA	CTGCGGATAA	GTTACTTTCA
Finale	GATTGAATAG	GAGTACTTCA	TTGGCGGAGA	CTGCGGATAA	GTTACTTTCA
Frission	GGTGTTTCGG	GTTATGTAAG	CAAGCCAACA	ATGTATGAAA	TGGATGCGAT
Finale	GGTGTTTCGG	GTTATGTAAG	CAAGCCAACA	ATGTATGAAA	TGGATGCGAT
Frission	CATGGAAGCT	ACAATGAACC	TGAGTGAGAA	TTGTAAGATT	GGTGAATCG
Finale	CATGGAAGCT	ACAATGAACC	TGAGTGAGAA	TTGTAAGATT	GGTGAATCG
Frission	TTTACAAGGC	TAATATAGAT	GGTAGAGTTT	TAGCAGTGAA	AAAAATCAAG
Finale	TTTACAAGGC	TAATATAGAT	GGTAGAGTTT	TAGCAGTGAA	AAAAATCAAG
Frission	AAAGATGCTT	CTGAGGAGCT	GAAAATTGTG	CAGAAGGTAA	ATCATGGAAA
Finale	AAAGATGCTT	CTGAGGAGCT	GAAAATTGTG	CAGAAGGTAA	ATCATGGAAA
Frission	TCTTGTGAAA	CTTATGGGTG	TGCTTCCGA	CAACGATGGA	AACGTGTTCC
Finale	TCTTGTGAAA	CTTATGGGTG	TGCTTCCGA	CAACGATGGA	AACGTGTTCC
Frission	TTGTTTACGA	GTATGCTGAA	AATGGATCAC	TTGATGAGTG	GTGTTCTCA
Finale	TTGTTTACGA	GTATGCTGAA	AATGGATCAC	TTGATGAGTG	GTGTTCTCA
Frission	GAGTGTGCA	AAACTTCGAA	CTCGTGGTC	TCGCTTACAT	GGTCTCAGAG
Finale	GAGTGTGCA	AAACTTCGAA	CTCGTGGTC	TCGCTTACAT	GGTCTCAGAG
Frission	AATAACAGTA	GCAGTGGATG	TTGCAGTTGG	TTTGCATATC	ATGCATGAAC
Finale	AATAACAGTA	GCAGTGGATG	TTGCAGTTGG	TTTGCATATC	ATGCATGAAC
Frission	ATACTTACCC	AAGAATAATC	CACAGAGACA	TCACAACAAG	TAATATCCTT
Finale	ATACTTACCC	AAGAATAATC	CACAGAGACA	TCACAACAAG	TAATATCCTT
Frission	CTGATTTCAA	ACTTTAAGGC	CAAGATAGCG	AATTTTTCAA	TGGCCAGAAG
Finale	CTGATTTCAA	ACTTTAAGGC	CAAGATAGCG	AATTTTTCAA	TGGCCAGAAG
Frission	TTCAACAAAT	TCCATGATGC	CGAAAAATCGA	TGTTTTCGCT	TTTGGGGTGG
Finale	TTCAACAAAT	TCCATGATGC	CGAAAAATCGA	TGTTTTCGCT	TTTGGGGTGG
Frission	TTCTGATTGA	GTTGCTTACC	GGCAAGAAAAG	CGATAACAAC	GATGGAAAAT
Finale	TTCTGATTGA	GTTGCTTACC	GGCAAGAAAAG	CGATAACAAC	GATGGAAAAT
Frission	GGCGAGGTGG	TTATTCTGTG	GAAGGATTTC	TGGAAGATTT	TTGATCTAGA
Finale	GGCGAGGTGG	TTATTCTGTG	GAAGGATTTC	TGGAAGATTT	TTGATCTAGA
Frission	AGGGAATAGA	GAAGAGAGCT	TAAGAAAATG	GATGGATCCT	AAGCTAGAGA
Finale	AGGGAATAGA	GAAGAGAGCT	TAAGAAAATG	GATGGATCCT	AAGCTAGAGA

Frison	<u>ATTTTATCC TATTGATAAT GCTCTTAGTT TGGCTTCTTT GGCAGTGAAT</u>
Finale	<u>ATTTTATCC TATTGATAAT GCTCTTAGTT TGGCTTCTTT GGCAGTGAAT</u>
Frison	<u>TGTACTGCAG ATAAATCAIT GTCAAGACCA AGCATTGCAG AAATTGTTCT</u>
Finale	<u>TGTACTGCAG ATAAATCAIT GTCAAGACCA AGCATTGCAG AAATTGTTCT</u>
Frison	<u>TTGCTTTTCT CTTCCTCAATC AATCATCATC TGAACCAATG TTGAAAGAT</u>
Finale	<u>TTGCTTTTCT CTTCCTCAATC AATCATCATC TGAACCAATG TTGAAAGAT</u>
Frison	<u>CCTTGACATC TGGTTTAGAT GTTGAAGCTA CTCATGTGT TACTTCTATA</u>
Finale	<u>CCTTGACATC TGGTTTAGAT GTTGAAGCTA CTCATGTGT TACTTCTATA</u>
Frison	<u>GTAGCTCGTT GATATTCATT CAAGTGAAGG TAACACTGAA TCAATGCTTC</u>
Finale	<u>GTAGCTCGTT GATATTCATT CAAGTGAAGG TAACACTGAA TCAATGCTTC</u>
Frison	<u>AGTTTCTTAT ATTCAAGATG GTTACTTTGT TTAGTTGATT ATTGATTACA</u>
Finale	<u>AGTTTCTTAT ATTCAAGATG GTTACTTTGT TTAGTTGATT ATTGATTACA</u>
Frison	<u>TCCTTATGTG TGGAACTATA TGGTTATTTT AATTAAGGGA ATTCTCTAA</u>
Finale	<u>TCCTTATGTG TGGAACTATA TGGTTATTTT AATTAAGGGA ATTCTCTAA</u>
Frison	<u>ATTTCATTTT TCCATGTT SEQ ID NO: 13</u>
Finale	<u>ATTTCATTTT TCCATGTT SEQ ID NO: 13</u>

* Nucleotide differences are shaded black and the coding region is underlined